

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/686, 835A
Source: JFW16
Date Processed by STIC: 09/22/2005

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/686,835A

DATE: 09/22/2005

TIME: 15:15:14

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\09222005\J686835A.raw

4 <110> APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
 6 <120> TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
 7 HEPATITIS C VIRUS
 9 <130> FILE REFERENCE: 13/083
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/686,835A
C--> 11 <141> CURRENT FILING DATE: 2003-10-16
 11 <150> PRIOR APPLICATION NUMBER: 10/029,907
 12 <151> PRIOR FILING DATE: 2001-12-21
 14 <150> PRIOR APPLICATION NUMBER: 60/257,857
 15 <151> PRIOR FILING DATE: 2000-12-22
 17 <160> NUMBER OF SEQ ID NOS: 28
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 8639
 23 <212> TYPE: DNA
 24 <213> ORGANISM: HCV
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1803)...(8408)
 30 <400> SEQUENCE: 1
 31 ggccagcccc cgattgggg cgacactcca ccatagatca ctccccctgtg aggaactact 60
 32 gtcttcacgc agaaaagcgtc tagccatggc gtttagtatga gtgtcggtc gcctccagga 120
 33 cccccccctcc cgggagagcc atagtggtct gcggaaccgg tgagtacacc ggaattgcc 180
 34 ggacgaccgg gtccttctt gnatcaaccc gctcaatgcc tggagatttg ggcgtgcccc 240
 35 cgcgagactg ctagccgagt agtgttgggt cgcgaaaggc cttgtggta cgcctgata 300
 36 ggtgcttgcg agtgcggcgg gaggtctcg agaccgtc acatgagcac gaatcctaaa 360
 37 cctcaaagaa aaaccaaagg ggcgcgcattt attgaacaag atggattgca cgcaggctt 420
 38 cccggcgctt gggtgagag gctatcgcc tatgactggg cacaacagac aatccgctgc 480
 39 tctgatgccg ccgtgtccg gctgtcagcg cagggcgcc cggttcttt tgtcaagacc 540
 40 gacctgtccg gtgcctgaa tgaactgcag gacgaggcag cgcggctatc gtggctggcc 600
 41 acgacggcgc ttccctgcg agctgtgctc gacgttgtca ctgaagcggg aaggactgg 660
 42 ctgctattgg ggcgaagtgc gggcgaggat ctcctgtcat ctcacccgtc tcctgcccag 720
 43 aaagtatcca tcatggctga tcaatgcgg cggctgcata cgcttgcattt ggctacccgtc 780
 44 ccattcgacc accaagcgaa acatcgcatc gagcggcac gtactcgat ggaagccgg 840
 45 cttgtcgatc aggtatctt ggacgaagag catcaggggc tcgcgcgcagc cgaactgttc 900
 46 gccaggctca aggccgcgcattt gcccgcggc gaggatctcg tcgtgaccca tggcgatgcc 960
 47 tgcttgcga atatcatggt gaaaaatggc cgctttctg gattcatcga ctgtggccgg 1020
 48 ctgggtgtgg cggaccgcta tcaggacata gcgttggcta cccgtgatat tgctgaagag 1080
 49 ctggcgccgc aatggctga ccgccttcctc gtgtttacg gtatgcggc tcccgattcg 1140
 50 cagcgcatcg ccttctatcg ctttcttgcg gagttcttctt gagttcgccgc ccagatgtta 1200
 51 acagaccaca acggttccccc tctagcggga tcaattccgc cccccccctt aacgttactg 1260
 52 gccaagccg ctttggataa ggcgggtgtg cgtttgtcta tatgttattt tccaccat 1320
 53 tgccgtcttt tggcaatgtg agggcccgga aacctggccc tgcgtttttt acgagcattc 1380

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54	ctaggggtct	ttcccccctc	gccaaggaa	tgcaaggct	gttgaatgtc	gtgaaggaag	1440
55	cagtccctct	ggaagcttct	tgaagacaaa	caacgtctgt	agcgaccctt	tgcagggcagc	1500
56	gaaacccccc	acctggcgac	aggtgcctct	gcccccaaaa	gccacgtgt	taagatacac	1560
57	ctgcaaaggc	ggcacaaaccc	cagtgcacg	ttgtgagttg	gatagttgtg	gaaagagtca	1620
58	aatggctctc	ctcaagcgta	ttcaacaagg	ggctgaagga	tgcccagaag	gtacccatt	1680
59	gtatgggatc	tcatctgggg	cctcggtca	catgcattac	atgtgtttag	tcgaggttaa	1740
60	aaaacgtcta	ggccccccga	accacgggaa	cgtggtttc	ctttgaaaaa	cacgataata	1800
61	cc atg gac	cgg gag atg	gca gca tcg	tgc gga ggc	gct ttc gta	1847	
62	Met Asp Arg	Glu Met Ala	Ala Ser Cys	Gly Gly Ala	Val Phe Val		
63	1	5	10	15			
65	ggt ctg ata ctc	ttg acc ttg	tca ccg cac	tat aag ctg	ttc ctc gct	1895	
66	Gly Leu Ile	Leu Leu Thr	Leu Ser Pro	His Tyr Lys	Leu Phe Leu Ala		
67	20	25	30				
69	agg ctc ata tgg	tgg tta caa	tat ttt atc	acc agg gcc gag	gca cac	1943	
70	Arg Leu Ile Trp	Trp Leu Gln	Tyr Phe Ile	Thr Arg Ala	Glu Ala His		
71	35	40	45				
73	ttg caa gtg	tgg atc ccc	ccc ctc aac	gtt cgg ggg ggc	cgc gat gcc	1991	
74	Leu Gln Val Trp	Ile Pro Pro	Leu Asn Val	Arg Gly Gly Arg	Asp Ala		
75	50	55	60				
77	gtc atc ctc	ctc acg tgc	gcg atc cac	cca gag cta	atc ttt acc atc	2039	
78	Val Ile Leu	Leu Thr Cys	Ala Ile His	Pro Glu Leu	Ile Phe Thr Ile		
79	65	70	75				
81	acc aaa atc ttg	ctc gcc ata ctc	ggt cca ctc atg	gtg ctc cag	gct	2087	
82	Thr Lys Ile	Leu Leu Ala	Ile Leu Gly	Pro Leu Met	Val Leu Gln Ala		
83	80	85	90	95			
85	ggt ata acc aaa	gtg ccg tac ttg	gtg cgc gca	cac ggg ctc	att cgt	2135	
86	Gly Ile Thr Lys	Val Pro Tyr	Phe Val Arg	Ala His Gly	Ile Arg		
87	100	105	110				
89	gca tgc atg	ctg gtg cgg	aag gtt gct	ggg ggt cat	tat gtc caa atg	2183	
90	Ala Cys Met	Leu Val Arg	Lys Val Ala	Gly Gly His	Tyr Val Gln Met		
91	115	120	125				
93	gct ctc atg	aag ttg gcc	gca ctg aca	ggt acg tac	gtt tat gac cat	2231	
94	Ala Leu Met	Lys Leu Ala	Ala Leu Thr	Gly Thr Tyr Val	Tyr Asp His		
95	130	135	140				
97	ctc acc cca	ctg cgg gac	tgg gcc cac	gct ggc cta	cga gac ctt gcg	2279	
98	Leu Thr Pro	Leu Arg Asp	Trp Ala His	Ala Gly Leu	Arg Asp Leu Ala		
99	145	150	155				
101	gtg gca gtt	gag ccc gtc	gtc ttc tct	gat atg gag	acc aag gtt atc	2327	
102	Val Ala Val	Glu Pro Val	Val Phe Ser	Asp Met Glu	Thr Lys Val Ile		
103	160	165	170	175			
105	acc tgg ggg	gca gac acc	gct gcg tgc	tgt ggg gac	atc atc ttg ggc	2375	
106	Thr Trp Gly	Ala Asp Thr	Ala Ala Cys	Gly Asp Ile	Ile Leu Gly Leu		
107	180	185	190				
109	ccc gtc tcc	gcc cgc agg	ggg agg gag	ata cat ctg	gga ccg gca gac	2423	
110	Pro Val Ser	Ala Arg Arg	Gly Arg Glu	Ile His Leu	Gly Pro Ala Asp		
111	195	200	205				
113	agc ctt gaa	ggg cag ggg	tgg cga ctc	ctc gct att	acg gcc tac	2471	
114	Ser Leu Glu	Gly Gln Gly	Trp Arg Leu	Leu Ala Pro	Ile Thr Ala Tyr		
115	210	215	220				

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117	tcc	caa	cag	acg	cga	ggc	cta	ctt	ggc	tgc	atc	atc	act	agc	ctc	aca	2519	
118	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr		
119	225				230						235							
121	ggc	cgg	gac	agg	aac	cag	gtc	gag	ggg	gag	gtc	caa	gtg	gtc	tcc	acc	2567	
122	Gly	Arg	Asp	Arg	Asn	Gln	Val	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr		
123	240				245						250					255		
125	gca	aca	caa	tct	ttc	ctg	gcg	acc	tgc	gtc	aat	ggc	gtg	tgt	tgg	act	2615	
126	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr		
127					260				265			265			270			
129	gtc	tat	cat	gtt	gcc	ggc	tca	aag	acc	ctt	gcc	ggc	cca	aag	ggc	cca	2663	
130	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro		
131					275				280			280			285			
133	atc	acc	caa	atg	tac	acc	aat	gtg	gac	cag	gac	ctc	gtc	ggc	tgg	caa	2711	
134	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln		
135				290				295			300							
137	gcg	ccc	ccc	ggg	gcg	cgt	tcc	ttg	aca	cca	tgc	acc	tgc	ggc	agc	tcg	2759	
138	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser		
139				305			310			315								
141	gac	ctt	tac	ttg	gtc	acg	agg	cat	gcc	gat	gtc	att	ccg	gtg	cgc	cgg	2807	
142	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg		
143				320			325			330			335					
145	cgg	ggc	gac	agg	ggg	agg	cta	ctc	tcc	ccc	agg	ccc	gtc	tcc	tac	2855		
146	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr		
147				340			345			345			350					
149	ttg	aag	ggc	tct	tcg	ggc	ggt	cca	ctg	ctc	tgc	ccc	tgc	ggg	cac	gtc	2903	
150	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala		
151				355			360			360			365					
153	gtg	ggc	atc	ttt	cg	gct	gcc	gt	tgc	acc	cga	ggg	gtt	g	g	g	2951	
154	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala		
155				370			375			380								
157	gtg	gac	ttt	gt	ccc	gtc	gag	tct	atg	gaa	acc	act	atg	cg	tcc	ccg	2999	
158	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro		
159				385			390			395								
161	gtc	tcc	acg	gac	aac	tcg	tcc	cct	ccg	gcc	gta	ccg	cag	aca	tcc	cag	3047	
162	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	Gln	Thr	Phe	Gln		
163				400			405			410			415					
165	gtg	gcc	cat	cta	cac	gcc	cct	act	ggt	agc	ggc	aag	agc	act	aag	gt	3095	
166	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val		
167				420			425			425			430					
169	ccg	gct	g	tat	gca	gcc	caa	ggg	tat	aag	gt	ctt	gtc	ctg	aac	ccg	3143	
170	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro		
171				435			440			440			445					
173	tcc	gtc	gcc	gcc	acc	cta	ggt	ttc	ggg	g	cg	tat	atg	tct	aag	gca	cat	3191
174	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His		
175				450			455			460								
177	ggt	atc	gac	cct	aac	atc	aga	acc	ggg	gta	agg	acc	atc	acc	acg	ggt	3239	
178	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly		
179				465			470			475								
181	gcc	ccc	atc	acg	tac	tcc	acc	tat	ggc	aag	ttt	ctt	gcc	gac	ggt	ggt	3287	

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182	Ala	Pro	Ile	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly
183	480			485				490				495				
185	tgc	tct	ggg	ggc	gcc	tat	gac	atc	ata	ata	tgt	gat	gag	tgc	cac	tca
186	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser
187					500				505				510			
189	act	gac	tcg	acc	act	atc	ctg	ggc	atc	ggc	aca	gtc	ctg	gac	caa	gcg
190	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala
191					515				520				525			
193	gag	acg	gct	gga	gcg	cga	ctc	gtc	gtg	ctc	gcc	acc	gct	acg	cct	ccg
194	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro
195					530			535				540				
197	gga	tcg	gtc	acc	gtg	cca	cat	cca	aac	atc	gag	gag	gtg	gct	ctg	tcc
198	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser
199					545			550				555				
201	agc	act	gga	gaa	atc	ccc	ttt	tat	ggc	aaa	gcc	atc	ccc	atc	gag	acc
202	Ser	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Thr
203	560				565				570				575			
205	atc	aag	ggg	ggg	agg	cac	ctc	att	ttc	tgc	cat	tcc	aag	aag	aaa	tgt
206	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys
207					580			585				590				
209	gat	gag	ctc	gcc	gcg	aag	ctg	tcc	ggc	ctc	aat	gct	gta	gca		3527
210	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	Leu	Asn	Ala	Val	Ala
211					595			600				605				
213	tat	tac	cg	ggc	ctt	gat	gta	tcc	gtc	ata	cca	act	agc	gga	gac	gtc
214	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	Thr	Ser	Gly	Asp	Val
215					610			615				620				
217	att	gtc	gta	gca	acg	gac	gct	cta	atg	acg	ggc	ttt	acc	ggc	gat	ttc
218	Ile	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	Phe	Thr	Gly	Asp	Phe
219					625			630				635				
221	gac	tca	gtg	atc	gac	tgc	aat	aca	tgt	gtc	acc	cag	aca	gtc	gac	ttc
222	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe
223	640				645				650				655			
225	agc	ctg	gac	ccg	acc	ttc	acc	att	gag	acg	acg	acc	gtg	cca	caa	gac
226	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp
227					660			665				670				
229	gcg	gtg	tca	cgc	tcg	cag	cg	cga	ggc	agg	act	ggt	agg	ggc	agg	atg
230	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Met
231					675			680				685				
233	ggc	att	tac	agg	ttt	gtg	act	cca	gga	gaa	cg	ccc	tcg	ggc	atg	ttc
234	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe
235					690			695				700				
237	gat	tcc	tcg	gtt	ctg	tgc	gag	tgc	tat	gac	g	ggc	tgt	gct	tgg	tac
238	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr
239					705			710				715				
241	gag	ctc	acg	ccc	gcc	gag	acc	tca	gtt	agg	ttg	cg	g	ct	ta	ac
242	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn
243	720				725						730				735	
245	aca	cca	ggg	ttg	ccc	gtc	tgc	cag	gac	cat	ctg	gag	ttc	tgg	gag	agc
246	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser

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247	740	745	750	
249	gtc ttt aca ggc ctc acc cac ata gac gcc cat ttc ttg tcc cag act			4103
250	Val Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr			
251	755	760	765	
253	aag cag gca gga gac aac ttc ccc tac ctg gta gca tac cag gct acg			4151
254	Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr			
255	770	775	780	
257	gtg tgc gcc agg gct cag gct cca cct cca tcg tgg gac caa atg tgg			4199
258	Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp			
259	785	790	795	
261	aag tgt ctc ata cgg cta aag cct acg ctg cac ggg cca acg ccc ctg			4247
262	Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu			
263	800	805	810	815
265	ctg tat agg ctg gga gcc gtt caa aac gag gtt act acc aca cac ccc			4295
266	Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Thr His Pro			
267	820	825	830	
269	ata acc aaa tac atc atg gca tgc atg tcg gct gac ctg gag gtc gtc			4343
270	Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val			
271	835	840	845	
273	acg agc acc tgg gtg ctg gta ggc gga gtc cta gca gct ctg gcc gcg			4391
274	Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala			
275	850	855	860	
277	tat tgc ctg aca aca ggc agc gtg gtc att gtg ggc agg atc atc ttg			4439
278	Tyr Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu			
279	865	870	875	
281	tcc gga aag ccg gcc atc att ccc gac agg gaa gtc ctt tac cgg gag			4487
282	Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu			
283	880	885	890	895
285	ttc gat gag atg gaa gag tgc gcc tca cac ctc cct tac atc gaa cag			4535
286	Phe Asp Glu Met Glu Glu Cys Ala Ser His Leu Pro Tyr Ile Glu Gln			
287	900	905	910	
289	gga atg cag ctc gcc gaa caa ttc aaa cag aag gca atc ggg ttg ctg			4583
290	Gly Met Gln Leu Ala Glu Gln Phe Lys Gln Lys Ala Ile Gly Leu Leu			
291	915	920	925	
293	caa aca gcc acc aag caa gcg gag gct gct gct ccc gtg gtg gaa tcc			4631
294	Gln Thr Ala Thr Lys Gln Ala Glu Ala Ala Ala Pro Val Val Glu Ser			
295	930	935	940	
297	aag tgg cgg acc ctc gaa gcc ttc tgg gcg aag cat atg tgg aat ttc			4679
298	Lys Trp Arg Thr Leu Glu Ala Phe Trp Ala Lys His Met Trp Asn Phe			
299	945	950	955	
301	atc agc ggg ata caa tat tta gca ggc ttg tcc act ctg cct ggc aac			4727
302	Ile Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn			
303	960	965	970	975
305	ccc gcg ata gca tca ctg atg gca ttc aca gcc tct atc acc agc ccg			4775
306	Pro Ala Ile Ala Ser Leu Met Ala Phe Thr Ala Ser Ile Thr Ser Pro			
307	980	985	990	
309	ctc acc acc caa cat acc ctc ctg ttt aac atc ctg ggg gga tgg gtg			4823
310	Leu Thr Thr Gln His Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val			
311	995	1000	1005	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 882,1489
Seq#:3; Xaa Pos. 882,1489

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:631 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:635 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:4489
M:341 Repeated in SeqNo=2
L:1237 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:1348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:880
M:341 Repeated in SeqNo=3